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DESCRIPTION

RECOMBINANT VIRUS VECTOR ORIGINATING IN HHV-6
OR HHV-7, METHOD OF PRODUCING THE SAME,
METHOD OF TRANSFORMING HOST CELL USING THE
SAME, HOST CELL TRANSFORMED THEREBY AND GENE
THERAPY METHOD USING THE SAME

TECHNICAL FIELD

The present invention relates to a recombinant virus and a recombinant virus vector, and more specifically to a recombinant virus, and a recombinant virus vector, originating in HHV-6 and HHV-7, which are members of the herpesvirus.

The present invention also relates to a producing method of such a recombinant virus and recombinant virus vector. The invention also relates to a method of transforming a host cell using such a recombinant virus and recombinant virus vector. Further, the invention relates to a host cell transformed by such a recombinant

virus and recombinant virus vector. The invention also relates to a gene therapy method using such a recombinant virus and recombinant virus vector.

BACKGROUND ART

Accumulation of knowledge and various technological advances in molecular biology and molecular genetics have greatly contributed to the recent progress in life science, providing rich information on various living phenomena.

Currently, there have been ongoing active research and development in various fields of life science, with particular interest in the analysis of gene functions. This has led to the development of techniques and vectors for introducing isolated genes into cells and individual living organisms.

For medical applications, there have been developed various types of vectors used to introduce genes into mammalian cells. Among these vectors, vectors using viruses (virus vectors) have drawn many interests.

Virus vectors have advantages over other known vectors in introducing a foreign gene into a cell for protein expression. The central idea underlying the gene transfer using the virus vector is to introduce a foreign gene into an infected cell and transform the cell with the

foreign gene under control of promoter sequences, taking advantage of the infectious capacity of the virus (productive infection, latent infection, abortive infection).

Conventional transfection techniques include non-viral methods. Examples of non-viral methods include: simple addition of a target gene construct as free DNA; incubation with a complex of target DNA and a specific protein that is designed to uptake the DNA into a target cell; and incubation with target DNA that is contained in infected genes that are encapsulated by liposome and other lipids. However, these non-viral transfection techniques suffer from poor efficiency, and the expression efficiency of introduced genes is generally poor.

One conventional transfection technique uses recombinant viruses, and recombinant virus vectors, that are manipulated to include essential target genes, can infect target cells, and therefore enables the target genes to be expressed in the cells. Various types of viruses, such as retrovirus, adenovirus, and adeno-associated virus are used for this purpose. However, these viruses have the following drawbacks.

For example, the retrovirus is carcinogenic, and its carcinogenicity in a gene therapy has been reported. Another drawback of the retrovirus is that it can

incorporate only small genes and is selective as to the types of cells that can be used to express the genes.

As to the adenovirus, it can trigger a strong allergic reaction when used in a gene therapy or the like. Some fatal cases in gene therapy have been reported. Further, the adenovirus suffers from poor efficiency when used to introduce genes into blood cells. It is therefore difficult to use the adenovirus as a vector.

The adeno-associated virus allows for introduction of only small genes, and its gene expression efficiency is poor. Another drawback of the adeno-associated virus is that it is difficult to produce a vector. Further, there is a potential risk of causing cancer when incorporated in the host gene.

To this date, eight broad kinds of viruses have been identified that belong to the herpesvirus family, taking into account only those infectious to humans. The herpesvirus is a large DNA virus, and is broadly classified into three sub families α , β , and γ according to the phylogenetic tree, with distinct biological characteristics in each sub family. For example, α -herpesvirus is a neurotropic virus that exhibits latency and reactivation in nerve cells, whereas γ -herpesvirus is oncogenic.

Human β -herpesvirus includes human cytomegalovirus (HCMV: human herpesvirus 5, HHV-5),

human herpesvirus 6 (HHV-6), and human herpesvirus (HHV-7).

Of these viruses, HHV-6 and HHV-7 in particular have drawn many interests as the candidates for virus vectors used for gene therapy (see Non-Patent Document 2, for example), since the disease caused by these viruses shows mild symptoms (see Non-Patent Document 1, for example).

Using the herpesvirus, and HHV-6 and HHV-7 in particular as a recombinant virus and a recombinant virus vector has certain advantages, which include low pathogenicity, ease of gene introduction into blood cells such as the T cell and macrophage, and introduction of relatively large genes.

Using HHV-6 as a recombinant virus or a recombinant virus vector is advantageous in the following respects. First, it allows for gene introduction into a macrophage, which is difficult with other vectors. Further, since the gene can be introduced into the macrophage in latency, the allergic reaction seen with the adenovirus does not occur.

However, it is difficult to produce a recombinant virus, and a recombinant virus vector, that originates in HHV-6 or HHV-7, and, today, no method is available that can produce such viruses and vectors. One of the factors

that makes recombination of HHV-6 and HHV-7 difficult, beside technical factors, can be attributed to the characteristics of HHV-6 and HHV-7 genes.

The size of gene in HHV-6 and HHV-7 is smaller than that in HCMV, and HHV-6 and HHV-7 contain essentially no genes that are dispensable for the viral replication as observed in HCMV (see Non-Patent Documents 3 and 4, for example).

As a rule, use of a homologous recombination method to produce a recombinant virus or a recombinant virus vector of the herpesvirus requires destruction of one or more sites. However, the recombination sites that have been conventionally used for the preparation of HCMV recombinant viruses are not necessarily included in HHV-6 and HHV-7. Accordingly, development of a new method is needed for the preparation of a recombinant virus and a recombinant virus vector of HHV-6 and HHV-7.

As a virus vector originating in the herpesvirus, there has been proposed a foreign gene that is inserted in the genome of a herpes simplex virus under control of a promoter regulating region of the genome, and therefore serving as a vector for expressing foreign genes (see Patent Document 1, for example). There are also disclosed a DNA construct, a plasmid vector including a construct

useful for the expression of foreign genes, a recombinant virus produced by such a vector, and methods concerning these. However, these publications merely describe a herpes simplex virus type 1 (HSV-1) vector and a producing method thereof, and do not disclose anything about virus vectors originating in HHV-6 or HHV-7.

Herpes simplex virus type 1 (HSV-1) and HHV-6 or HHV-7 were evolved from a common ancestor, but completely differ from each other in gene structure. Further, the homology of gene sequences is low between these viruses, and the cellular tropism, which is very important in producing a vector or performing gene therapy, is totally different. Thus, in order to produce vectors originating in HHV-6 or HHV-7, a new technique needs to be developed that is different from that used for herpes simplex virus type 1 (HSV-1).

Other publications disclose results of using the herpesvirus vector. Specifically, there has been proposed a method in which malignant cells of hematopoietic cell lines are transformed to induce expression of foreign gene substances in the cells (for example, see Patent Publication 2). However, the publication merely describes herpes simplex virus type 1, and does not disclose anything about producing methods of HHV-6 or HHV-7 vectors, or side effects of the gene therapy.

[Patent Document 1] European Patent No. 176170

[Patent Document 2] Japanese Laid-Open PCT
Publication No. 11-513565

[Non-Patent Document 1] Clin. Microbiol. Rev., July,
1997, Vol. 10, No. 3, p.521-567

[Non-Patent Document 2] J. Virol. Meth., September
2002, Vol. 105, No. 2, p.331-341

[Non-Patent Document 3] Yuji Isegawa et al., J.
Virol., October 1999, Vol. 73, No. 10, p.8053-8063

[Non-Patent Document 4] A. George Megaw et al.,
Virology, 1998, Vol. 244, p.119-132

An object of the present invention is to provide a virus vector that (i) allows for insertion of an exogenous nucleotide sequence, (ii) can easily transfect a host cell of mammals, (iii) allows a gene encoded by the exogenous nucleotide sequence to be expressed in the host cell, (iv) has a low risk of pathogenicity, and therefore (v) is suitable for gene therapy of mammals.

Another object of the present invention is to provide a virus vector producing method for easily and safely producing a virus vector that (i) allows for insertion of an exogenous nucleotide sequence, (ii) can easily transfect a host cell of mammals, (iii) allows a gene encoded by the exogenous nucleotide sequence to be expressed in the host cell, (iv) has a low risk of pathogenicity, and

therefore (v) is suitable for gene therapy of mammals.

Another object of the present invention is to provide a host cell transforming method for transforming a host cell with a virus vector that (i) easily allows for transfection of a mammalian host cell with an exogenous nucleotide sequence, (ii) allows a gene encoded by the exogenous nucleotide sequence to be expressed in the host cell, (iii) has a low risk of pathogenicity, and therefore (iv) is suitable for gene therapy of mammals.

Another object of the present invention is to provide a transformed host cell that (i) is transformed by a virus vector with the insertion of an exogenous nucleotide sequence, (ii) allows a gene encoded by the exogenous nucleotide sequence to be expressed in the host cell, (iii) has a low risk of pathogenicity, and therefore (iv) can suitably be used for gene therapy and cell therapy.

Another object of the present invention is to provide a gene therapy method for mammals using a virus vector that (i) easily allows for transfection of a mammalian host cell with an exogenous nucleotide sequence, (ii) allows a gene encoded by the exogenous nucleotide sequence to be expressed in the host cell, and (iii) has a low risk of pathogenicity.

Another object of the present invention is to develop a gene therapy method, a recombinant virus, and a

recombinant virus vector with the use of viruses which do not pose problems of conventionally used viruses, including poor gene introduction efficiency, instable gene expression, and a potential risk of causing cancer.

DISCLOSURE OF INVENTION

The inventors of the present invention diligently worked to solve the foregoing problems by contemplating that HHV-6 or HHV-7, which produces fairly mild symptoms and latently infects nearly 100% of healthy adult individuals may be suitably used as a virus vector for gene therapy.

Specifically, in order to make a recombinant virus, the inventors of the present invention conducted trial and error experiments in an effort to find dispensable regions that can be replaced with drug resistant genes, as will be described later in Examples.

As a result, the inventors of the present invention found a gene cluster that is non-essential and therefore dispensable for the replication and latency of human herpesvirus 6 (HHV-6) and human herpesvirus 7 (HHV-7), as will be described later in Examples.

Based on this finding, the inventors of the present invention accomplished the present invention by finding that insertion of an exogenous nucleotide sequence in a

specific region of HHV-6 or HHV-7 does not impair functions of HHV-6 or HHV-7 as a virus vector, thereby enabling production of a recombinant virus and recombinant virus vector originating in HHV-6 and HHV-7, which is very difficult with conventional techniques.

Specifically, a recombinant virus vector of the present invention originates in HHV-6 and includes an exogenous nucleotide sequence in a portion corresponding to at least one region selected from the group consisting of U2, U3, U4, U5, U6, U7, U8, U24, and U25 regions of HHV-6.

It is preferable that the portion exist between nucleotide numbers 9041 and 17446, or between nucleotide numbers 36250 and 37775 of a HHV-6 DNA sequence as represented by SEQ ID NO: 1. It is also preferable that the recombinant virus vector comprises H6R28 virus or H6R24-25 virus.

A recombinant virus vector of the present invention may originate in HHV-7 and include an exogenous nucleotide sequence in a portion corresponding to at least one region selected from the group consisting of U2, U3, U4, U7, U8, U24, U24a, and U25 regions of HHV-7.

It is preferable that the portion exists between nucleotide numbers 10558 and 18483, or between nucleotide numbers 34744 and 36118 of a HHV-7 DNA

sequence as represented by SEQ ID NO: 2. It is also preferable that the recombinant virus vector comprises H7R28 virus or H7R24-25 virus.

The exogenous nucleotide sequence may be a DNA sequence and/or RNA sequence.

The exogenous nucleotide sequence may encode at least one kind of substance selected from the group consisting of a bacterial artificial chromosome (BAC), cytokine gene, ribozyme, interference RNA, immunological co-stimulator molecule, signal transduction molecule, enzyme, and chemical attractant.

Further, the exogenous nucleotide sequence may be used for gene therapy of mammals. The exogenous nucleotide sequence may include a nucleotide sequence that encodes a marker gene.

A producing method of a recombinant virus of the present invention originates in HHV-6, and the method includes the step of inserting an exogenous nucleotide sequence in a portion corresponding to at least one region selected from the group consisting of U2, U3; U4, U5, U6, U7, U8, U24, and U25 regions of HHV-6.

It is preferable that, in the step of inserting an exogenous nucleotide sequence, the exogenous nucleotide sequence be inserted between nucleotide numbers 9041 and 17446, or between nucleotide numbers 36250 and

37775 of a HHV-6 DNA sequence as represented by SEQ ID NO: 1.

In the step of inserting an exogenous nucleotide sequence, homologous recombination may be carried out between a HHV-6 DNA sequence and a DNA sequence that is amplified with a primer set of a sequence represented by SEQ ID NO: 3-4 and a sequence represented by SEQ ID NO: 5-6, or a primer set of a sequence represented by SEQ ID NO: 36-37 and a sequence represented by SEQ ID NO: 38-39.

A producing method of a recombinant virus vector of the present invention may originate in HHV-7, and the method may include the step of inserting an exogenous nucleotide sequence in a portion corresponding to at least one region selected from the group consisting of U2, U3, U4, U7, U8, U24, U24a, and U25 regions of HHV-7.

In the step of inserting an exogenous nucleotide sequence, the exogenous nucleotide sequence may be inserted between nucleotide numbers 10558 and 18483, or between nucleotide numbers 34744 and 36118 of a HHV-7 DNA sequence as represented by SEQ ID NO: 2.

In the step of inserting an exogenous nucleotide sequence, homologous recombination may be carried out between a HHV-7 DNA sequence and a DNA sequence that is amplified with a primer set of a sequence represented

by SEQ ID NO: 30-31 and a sequence represented by SEQ ID NO: 34-35, or a primer set of a sequence represented by SEQ ID NO: 40-41 and a sequence represented by SEQ ID NO: 42-43.

In the step of inserting an exogenous nucleotide sequence, the exogenous nucleotide sequence may be inserted inside a normal cell and/or an umbilical cord blood cell.

A transforming method of a host cell of the present invention transforms a host cell of a mammal with the recombinant virus vector of the invention, and the method includes the step of transforming, with the recombinant virus vector, a host cell of at least one kind of mammal selected from the group consisting of a human, a non-human primate, and a host that is open to HHV-6 or HHV-7 infection.

In the step of transforming a host cell, the method may transform, with the recombinant virus vector, at least one kind of host cell selected from the group consisting of a T cell, macrophage, peripheral-blood mononuclear cell, blood stem cell, liver cell, vascular endothelial cell, fibroblast, glial cell, astrocyte, CD4 positive T cell, CD8 positive T cell, dendritic cell, and natural killer cell.

A transformed host cell of the present invention is

obtained by the transforming method of the invention. A transformed host cell of the present invention may be used for gene therapy of mammals.

Further, the gene therapy may be for preventing human immunodeficiency virus (HIV) infection of a compromised cell caused by HIV, and/or for immunotherapy of cancer. The host cell may be derived from a mammal of the kind subjected to the gene therapy.

A gene therapy method of the present invention is for non-human mammals, and the method includes the step of administering the transformed cell of the invention.

A gene therapy method of the present invention is for non-human mammals, and the method may include the step of transforming, with a recombinant virus vector of claim 1 or 4, a host cell of a mammal in vivo at a multiplicity of infection (MOI) of 0.01 to 20.

A gene therapy method of the present invention may include the step of expressing a gene encoded by the exogenous nucleotide sequence included in the recombinant virus vector.

Additional objects, features, and strengths of the present invention will be made clear by the description below. Further, the advantages of the present invention will be evident from the following explanation in reference

to the drawings.

BRIEF DESCRIPTION OF DRAWINGS

Figure 1 is a schematic diagram representing a structure of a H6R28 genome.

Figure 2(A) is an electrophoretogram view representing results of PCR amplification between regions U2 and U8 of wild-type (wt) virus DNA and H6R28 virus DNA; Figure 2(B) is an electrophoretogram view of fragments obtained by digesting the PCR products of Figure 2(A) with restriction enzymes; Figure 2(C) is an electrophoretogram view representing results of PCR amplification that was performed to confirm an insertion position of an EGFP-puro cassette in H6R28 virus DNA; Figure 2(D) is an electrophoretogram view representing results of PCR amplification that was performed to amplify region U3 to U7 of wild-type (wt) virus DNA and H6R28 virus DNA.

Figure 3(A) is a graphical view representing an increase of the cells stained with anti-HHV-6 monoclonal antibody in cells infected with H6R28; Figure 3(B) is a graphical view representing changes in virus titer (the number of surviving cells) in the culture supernatant of the cells infected with H6R28.

Figure 4 is a schematic diagram representing a

structure of H6R24-25 genome.

Figure 5(A) is a graphical view representing an increase of anti-HHV-6 monoclonal antibody positive cells in cells infected with H6R24-25; Figure 5(B) is a graphical view representing changes in virus titer (the number of surviving cells) in the culture supernatant of cells infected with H6R24-25.

Figure 6(A) is a graphical view representing percentages of HHV-6 DNA positive cells in cells latently infected with H6R28; Figure 6(B) is a graphical view representing percentages of reactivated cells in cells latently infected with H6R28.

Figure 7(A) is a fluorescent micrograph view of macrophage latently infected with H6R28; Figure 7(B) is a fluorescent micrograph view of latently infected macrophage transfected with plasmid pU2-U8EGFP-puro; Figure 7(C) is a fluorescent micrograph view of reactivation-induced macrophage; Figure 7(D) is a fluorescent micrograph view of CBMCs infected with H6R28; Figure 7(E) is a fluorescent micrograph view of Molt-3 cells infected with H6R28; Figure 7(F) is a fluorescent micrograph view of HeLa cells infected with H6R28.

Figure 8(A) is a view showing the result of FACS on EGFP expression of natural killer cells uninfected with

H6R28; Figure 8(B) is a view showing the result of FACS on EGFP expression of natural killer cells infected with H6R28; and Figure 8(C) is a view summing the results shown in Figures 8(A) and 8(B).

Figure 9 is a fluorescent micrograph view showing the EGFP expression of astrocytes infected with H6R28.

Figure 10 is a view showing the result of FACS on EGFP expression of CD4 positive T cells infected with H6R28.

Figure 11 is a view showing the result of FACS on EGFP expression of CD8 positive T cells infected with H6R28.

Figure 12 is a view showing the result of FACS on EGFP expression of dendritic cells infected with H6R28.

Figure 13(A) is a schematic diagram representing the 5' RACE method used to examine functions of HCMV promoter during H6R28 latency; and Figure 13(B) is an electrophoretogram view showing fragments amplified by 5' RACE.

Figure 14 is a schematic diagram showing a structure of the H7R28 genome.

Figure 15(A) is a graphical view representing an increase in the cells stained with anti-HHV-7 monoclonal antibody in cells infected with H7R28; and Figure 15(B) is a graphical view representing changes in virus titer (the

number of surviving viruses) in the supernatant of cultured cells infected with H7R28.

Figure 16 is a schematic diagram showing a structure of the H7R24-25 genome.

Figure 17(A) is a graphical view representing an increase in the cells stained with anti-HHV-7 monoclonal antibody in cells infected with H7R24-25; and Figure 17(B) is a graphical view representing changes in virus titer (the number of surviving viruses) in the supernatant of cultured cells infected with H7R24-25.

Figure 18 is a view showing the result of FACS on EGFP expression of macrophages infected with H7R28.

Figure 19 is a view showing the result of FACS on EGFP expression of CD4 positive T cells infected with H7R28.

Figure 20 is a view showing the result of FACS on EGFP expression of dendritic cells infected with H7R28.

Figure 21 is a schematic diagram showing a structure of the H6R28 BAC genome.

Figure 22 is a fluorescent micrograph view of Molt-3 cells infected with H6R28 BAC.

Figure 23 is a schematic diagram showing a structure of the H7R28 BAC genome.

Figure 24 is a fluorescent micrograph view of SupT1 cells infected with H7R28 BAC.

BEST MODE FOR CARRYING OUT THE INVENTION

The present invention is now described in detail in the embodiment below.

<Definitions>

As used herein, HHV-6 refers to variants A and B of human herpesvirus 6.

As used herein, HHV-7 refers to human herpesvirus 7.

As used herein, a recombinant virus and a recombinant virus vector refer to a virus or a virus vector that is prepared by incorporating foreign genes in viral genes, and that causes either one of productive infection, latent infection/reactivation, and abortive infection when used to infect a host cell.

As used herein, a dispensable region refers to a viral gene region, the lack of which does not lead to a complete loss of the proliferating ability of the virus.

As used herein, an exogenous nucleotide sequence refers to a nucleic acid sequence other than those found in naturally occurring viral genes.

As used herein, latent infection refers to a situation where production of infectious virus is suspended with the viral genes retained in the virus.

As used herein, infection refers to entry of virus into a cell, and it includes productive infection, latent

infection, and abortive infection.

As used herein, abortive infection refers to a situation where a virus that has entered a cell does not actively retain viral genes while no infectious virus is produced.

As used herein, gene therapy refers to therapy in which a cell is transformed by transfecting the cell with foreign genes. In a narrow sense, it includes cell therapy in which a cell that has been transformed ex vivo by gene transfection is returned to the living organism, and virus therapy in which a cell is infected with infectious virus in vivo in order to facilitate modification of the host cell by a resulting virus.

<HHV-6-Derived Recombinant Virus and Recombinant Virus Vector>

A recombinant virus and recombinant virus vector of the present invention are derived from HHV-6 and include an exogenous nucleotide sequence in a portion corresponding to at least one region selected from the group consisting of U2, U3, U4, U5, U6, U7, U8, U24, and U25 regions of HHV-6.

The U2 region of HHV-6 is an open reading frame (ORF) encoded by nucleotide number 10768 (start) to nucleotide number 9467 (end) of HHV-6 as represented by SEQ ID NO: 1, and it shares a common motif with the

US22 gene family of HCMV.

The U3 region of HHV-6 is an open reading frame (ORF) encoded by nucleotide number 12051 (start) to nucleotide number 10891 (end) of HHV-6 as represented by SEQ ID NO: 1, and it shares a common motif with the US22 gene family of HCMV.

The U4 region of HHV-6 is an open reading frame (ORF) encoded by nucleotide number 13883 (start) to nucleotide number 12276 (end) of HHV-6 as represented by SEQ ID NO: 1, and it has unknown functions.

The U5 region of HHV-6 is an open reading frame (ORF) encoded by nucleotide number 15333 (start) to nucleotide number 14002 (end) of HHV-6 as represented by SEQ ID NO: 1, and it has unknown functions.

The U6 region of HHV-6 is an open reading frame (ORF) encoded by nucleotide number 15395 (start) to nucleotide number 15652 (end) of HHV-6 as represented by SEQ ID NO: 1, and it has unknown functions.

The U7 region of HHV-6 is an open reading frame (ORF) encoded by nucleotide number 16802 (start) to nucleotide number 15678 (end) of HHV-6 as represented by SEQ ID NO: 1, and it shares a common motif with the US22 gene family of HCMV.

The U8 region of HHV-6 is an open reading frame (ORF) encoded by nucleotide number 18041 (start) to

nucleotide number 16806 (end) of HHV-6 as represented by SEQ ID NO: 1, and it shares a common motif with the US22 gene family of HCMV.

The U24 region of HHV-6 is an open reading frame (ORF) encoded by nucleotide number 36616 (start) to nucleotide number 36350 (end) of HHV-6 as represented by SEQ ID NO: 1, and it has unknown functions.

The U25 region of HHV-6 is an open reading frame (ORF) encoded by nucleotide number 38770 (start) to nucleotide number 37883 (end) of HHV-6 as represented by SEQ ID NO: 1, and it shares a common motif with the US22 gene family of HCMV.

The foregoing portions of HHV-6 may exist between nucleotide number 9041 and nucleotide number 17446, or between nucleotide number 36250 and nucleotide number 3777 of the DNA sequence of HHV-6 as represented by SEQ ID NO: 1. This is because nucleotide number 9041 to nucleotide number 17446 contains U2 region to U8 region of HHV-6, which were found to be dispensable as will be described later in Examples, and because nucleotide number 36250 to nucleotide number 3777 contains U24 region to U25 region of HHV-6, which were found to be dispensable as will be described later in Examples.

The foregoing portions of HHV-6 may exist between nucleotide number 10216 and nucleotide number 16547,

or between nucleotide number 36250 and nucleotide number 37775 of the DNA sequence of HHV-6 as represented by SEQ ID NO: 1. This is because nucleotide number 10216 to nucleotide number 16547 were experimentally confirmed to be dispensable as will be described later in Examples, and because nucleotide number 36250 to nucleotide number 37775 were experimentally confirmed to be usable for recombination, as will be described later in Examples.

A desirable exogenous nucleotide can easily be inserted in these portions in the manner described below. First, the HHV-6 DNA is cut at restriction enzyme cutting sites in these portions under appropriate conditions, using commercially available restriction enzymes. Then, the HHV-6 DNA is ligated under appropriate conditions to an exogenous nucleotide having complementary ends, using a commercially available ligase.

As to functions of US22 family genes, some information is available for human cytomegalovirus or mouse cytomegalovirus that belongs to β -herpes virus as does HHV-6 or HHV-7. However, no information is available for HHV-6 and HHV-7. The present invention, for the first time, analyzed functions of US22 family genes of HHV-6 and HHV-7 concerning their proliferation and latency.

The US22 family genes of HHV-6 and HHV-7 are merely classified according to a virtual motif on amino acid sequences whose functions are yet to be determined. As such, the fact that the genes belong to this family does not necessarily mean that their functions can be predicted. Further, there is no strong amino acid homology between homologous proteins of the HHV-6, HHV-7, and cytomegalovirus.

<HHV-7-Derived Recombinant Virus and Recombinant Virus Vector>

A recombinant virus and recombinant virus vector of the present invention may be derived from HHV-7 and may include an exogenous nucleotide sequence in a portion corresponding to at least one region selected from the group consisting of U2, U3, U4, U7, U8, U24, U24a, and U25 regions of HHV-7.

The U2 region of HHV-7 is an open reading frame (ORF) encoded by nucleotide number 11637 (start) to nucleotide number 10558 (end) of HHV-7 as represented by SEQ ID NO: 2, and it shares a common motif with the US22 gene family of HCMV.

The U3 region of HHV-7 is an open reading frame (ORF) encoded by nucleotide number 12953 (start) to nucleotide number 11799 (end) of HHV-7 as represented by SEQ ID NO: 2, and it shares a common motif with the

US22 gene family of HCMV.

The U4 region of HHV-6 is an open reading frame (ORF) encoded by nucleotide number 14603 (start) to nucleotide number 12975 (end) of HHV-7 as represented by SEQ ID NO: 2, and it is associated with exon 2 of U7.

Exon 1 (also known as U5) in the U7 region of HHV-7 is an open reading frame (ORF) encoded by nucleotide number 17324 (start) to nucleotide number 16348 (end) of HHV-7 as represented by SEQ ID NO: 2, and it shares a common motif with the US22 gene family of HCMV.

Exon 2 (also known as U7) in the U7 region of HHV-7 is an open reading frame (ORF) encoded by nucleotide 16266 (start) to nucleotide number 14628 (end) of HHV-7 as represented by SEQ ID NO: 2, and it is associated with the U4 region.

The U24 region of HHV-7 is an open reading frame (ORF) encoded by nucleotide number 34992 (start) to nucleotide number 34744 (end) of HHV-7 as represented by SEQ ID NO: 2, and it has unknown functions.

The U24a region of HHV-7 is an open reading frame (ORF) encoded by nucleotide number 35166 (start) to nucleotide number 34996 (end) of HHV-7 as represented by SEQ ID NO: 2, and it has unknown functions.

The U25 region of HHV-6 is an open reading frame (ORF) encoded by nucleotide number 36118 (start) to

nucleotide number 35156 (end) as represented by SEQ ID NO: 2, and it shares a common motif with the US22 gene family of HCMV.

The foregoing portions of HHV-7 may exist between nucleotide number 10558 and nucleotide number 18483, or between nucleotide number 34744 and nucleotide number 36118 of the DNA sequence of HHV-7 as represented by SEQ ID NO: 2. This is because nucleotide number 10558 to nucleotide number 18483 contains U2, U3, U4, U7, and U8 regions of HHV-7, which were found to be dispensable as will be described later in Examples, and because nucleotide number 34744 to nucleotide number 36118 contains U24, U24a, and U25 regions of HHV-7, which were found to be dispensable as will be described later in Examples.

The foregoing portions of HHV-7 may exist between nucleotide number 11631 and nucleotide number 17221, or between nucleotide number 34744 and nucleotide number 36118 of the DNA sequence of HHV-7 as represented by SEQ ID NO: 2. This is because nucleotide number 11631 to nucleotide number 17221 were experimentally confirmed to be dispensable as will be described later in Examples, and because nucleotide number 34744 to nucleotide number 36118 were experimentally confirmed to be usable for recombination,

as will be described later in Examples.

A desirable exogenous nucleotide can easily be inserted in these portions in the manner described below. First, the HHV-7 DNA is cut at restriction enzyme cutting sites in these portions under appropriate conditions, using commercially available restriction enzymes. Then, the HHV-7 DNA is ligated under appropriate conditions to an exogenous nucleotide having complementary ends, using a commercially available ligase.

<Exogenous Nucleotide Sequence>

The exogenous nucleotide sequence may be a DNA sequence and/or an RNA sequence. The DNA sequence may be a genomic DNA sequence or cDNA sequence.

Further, the exogenous nucleotide sequence may be a nucleotide sequence that encodes one or more substances selected from the group consisting of a bacterial artificial chromosome (BAC), a cytokine gene, a ribozyme, interference RNA, immunological co-stimulator molecule, and a chemical attractant.

Further, the exogenous nucleotide sequence may be a sequence used for gene therapy of mammals. Further, the exogenous nucleotide sequence may be a nucleotide sequence that encodes an immunoregulatory protein useful for a tumor treatment and/or immune treatment of mammals.

Further, the exogenous nucleotide sequence may include a nucleotide sequence that encodes a marker gene. The marker gene may be an antibiotic-resistant gene.

<Producing Method of Recombinant Virus and Recombinant Virus Vector>

A producing method of a recombinant virus and recombinant virus vector of the present invention is for producing a recombinant virus and recombinant virus vector derived from HHV-6, the method including the step of inserting an exogenous nucleotide sequence in a portion corresponding to at least one region selected from the group consisting of U2, U3, U5, U6, U7, U8, U24, and U25 regions of HHV-6.

The step of inserting an exogenous nucleotide sequence preferably includes the step of cutting the HHV-6 DNA under appropriate conditions at restriction enzyme cutting sites in the foregoing portion, using a commercially available restriction enzyme, and the step of ligating the HHV-6 DNA under appropriate conditions with an exogenous nucleotide having complementary ends, using a commercially available ligase. In this manner, with the commercially available restriction enzyme and ligase, a desirable exogenous nucleotide can easily be inserted in the foregoing portions.

The step of inserting an exogenous nucleotide

sequence may include the step of inserting an exogenous nucleotide sequence between nucleotide number 9041 and nucleotide number 17446 or between nucleotide number 36250 and nucleotide number 37775 of the DNA sequence of HHV-6 as represented by SEQ ID NO: 1. This is because nucleotide number 9041 to nucleotide number 17446 contains U2 region to U8 region of HHV-6, which were found to be dispensable as will be described later in Examples, and because nucleotide number 36250 to nucleotide number 37775 contains U24 region to U25 region of HHV-6, which were found to be dispensable as will be described later in Examples.

Further, the step of inserting an exogenous nucleotide sequence may include the step of inserting an exogenous nucleotide sequence between nucleotide number 10216 and nucleotide number 16547 or between nucleotide number 36250 and nucleotide number 37775 of the DNA sequence of HHV-6 as represented by SEQ ID NO: 1. This is because nucleotide number 10216 to nucleotide number 16547 were experimentally confirmed to be dispensable as will be described later in Examples, and because nucleotide number 36250 to nucleotide number 37775 were experimentally confirmed to be usable for recombination, as will be described later in Examples.

Further, the step of inserting an exogenous

nucleotide sequence may include the step of performing homologous recombination between a DNA sequence of HHV-6 and a DNA sequence amplified with a combination of primers having the sequences of SEQ ID NOs: 3 and 4 and primers having the sequences of SEQ ID NOs: 5 and 6, or a combination of primers having the sequences of SEQ ID NOs: 36 and 37 and primers having the sequences of SEQ ID NOs: 38 and 39.

[Table 1]

PRIMER	SEQ ID NO:	PRIMER SEQUENCE
U2 Xba I	3	5'- GCTCTAGACTGCCACGTGAGCGAAAGCATACAC -3'
U2 Afl II	4	5'- TTACTTAAGTCATCGGGGTCCTATCTTCGCAG -3'
U8 Bam HI	5	5'- CCGGATCCGAGTTAATGCATACATGGGAGGCCAGG -3'
U8 Eco RI	6	5'- CGGAATTCCTGTGTACCGTCATGGCTTGT -3'
U2R1	7	5'- GACATGCCTACGCGGCCTCACCGAG -3'
U2R2	8	5'- GGACGCGTGTAGAAACGGCCAACG -3'
U8F1	9	5'- GTACTAACATCATCACATGCGCGGAG -3'
U8F2	10	5'- GGGACTATTCAGATTCCTTACAGAG -3'
EGFPprim	11	5'- GACTCAGATCTCGAGCTCAAGCTTCG -3'
PACprim	12	5'- CCTTCTACGAGCGGCTCGGCTTCAC -3'
U3F	13	5'- ATGGAAACGACAAACAGCCGGCGTG -3'
U3R	14	5'- CTATCGAACTACGTCGTGCACGGC -3'
U4F	15	5'- CGGCACGTTGACCGCAGAGGATCTG -3'
U4R	16	5'- CTCCGGTGCTCCTGCAACCTGATGTC -3'
U5F	17	5'- GAAGTGGCAGTGCATCACTAACTGGC -3'
U5R	18	5'- CCATTCAGTTCGCCGGCACAGTCC -3'
U6F	19	5'- GCCAAATCTAGCTGCTGAGGTTCCC -3'
U6R	20	5'- CTGTTTGCGGTGCGTCTGGACGAAG -3'
U7F	21	5'- GAGGGCGGAAAGCGAGTCTTGTGTG -3'
U7R	22	5'- CATCCTCGAAGAATTGTCTTTTCGGG -3'
EGFP R1	23	5'- CGTAGCCTTCGGGCATGGCGGACTTG -3'
EGFP R2	24	5'- CCTTCAGCTCGATGCGGTTACCAGG -3'
RL-1	25	5'-CTTATGAGTATTTCTTCCAGGGTACTCGAGGCTGGGTAGT CCCCACCTTTCTAGATTTTTTTTTTTTTTTTTTTT-3'
N1	26	5'- GCTGGGTAGTCCCCACCTTTCTAGA -3'
N2	27	5'- CTTATGAGTATTTCTTCCAGGGTACTCGAG -3'
U24 Spe I	36	5'- GGACTAGTCAGATTTGTCATGTTAGTTTAATAGTCG -3'
U25 Eco RI	37	5'- GGAATTCCGCAAGATACGGACTATATTAAGCAGG -3'
U25 Mlu I	38	5'- CGACGCGTCCATTGCGTATGCAACCGACGATTCTC -3'
U25 Kpn I	39	5'- GGGGTACCCTGAGCCGGGCAGTTCATCGTTATGG -3'

A producing method of a recombinant virus and recombinant virus vector of the present invention is for producing a recombinant virus and recombinant virus vector derived from HHV-7, the method including the step of inserting an exogenous nucleotide sequence in a portion corresponding to at least one region selected from the group consisting of U2, U3, U4, U7, U8, U24, U24a, and U25 regions of HHV-7.

The step of inserting an exogenous nucleotide sequence preferably includes the step of cutting the HHV-7 DNA under appropriate conditions at restriction enzyme cutting sites in the foregoing portion, using a commercially available restriction enzyme, and the step of ligating the HHV-7 DNA under appropriate conditions with an exogenous nucleotide having complementary ends, using a commercially available ligase. In this manner, with the commercially available restriction enzyme and ligase, a desirable exogenous nucleotide can easily be inserted in the foregoing portions.

The step of inserting an exogenous nucleotide sequence may include the step of inserting an exogenous nucleotide sequence between nucleotide number 10558 and nucleotide number 18483 or between nucleotide number 34744 and nucleotide number 36118 of the DNA sequence of HHV-7 as represented by SEQ ID NO: 2. This

is because nucleotide number 10558 to nucleotide number 18483 contains U2, U3, U4, U7, and U8 regions of HHV-7, which were found to be dispensable as will be described later in Examples, and because nucleotide number 34744 to nucleotide number 36118 contains U24, U24a, and U25 regions of HHV-7, which were found to be dispensable as will be described later in Examples.

Further, the step of inserting an exogenous nucleotide sequence may include the step of inserting an exogenous nucleotide sequence between nucleotide number 1163 and nucleotide number 17221 or between nucleotide number 34744 and nucleotide number 36118 of the DNA sequence of HHV-7 as represented by SEQ ID NO: 2. This is because nucleotide number 1163 to nucleotide number 17221 were experimentally confirmed to be dispensable as will be described later in Examples, and because nucleotide number 34744 to nucleotide number 36118 were experimentally confirmed to be usable for recombination, as will be described later in Examples.

Note that, the step of inserting an exogenous nucleotide may include the step of inserting an exogenous nucleotide sequence inside a normal cell and/or a normal umbilical cord blood cell. A drawback of the adenovirus conventionally used to construct a recombinant virus vector is that construction of recombinant virus is

difficult unless it is performed inside HEK293 cell lines derived from kidney cancer cells. An advantage of a recombinant virus vector of the present invention, on the other hand, is that it can be constructed inside a normal cell, or more preferably inside a normal umbilical cord blood cell.

<Transformation Method of Host Cell>

A method for transforming a host cell of the present invention is for transforming a host cell of mammals with use of the recombinant virus and recombinant virus vector, and the method includes the step of transforming a host cell with the recombinant virus and recombinant virus vector at a multiplicity of infection (MOI) of 0.01 to 20.

The transformation step may include the step of transforming, with the recombinant virus and recombinant virus vector, a host cell derived from one or more kinds of mammals selected from the group consisting of a human, a non-human primate, and a host that is open to HHV-6 or HHV-7 infection.

Further, the transformation step may include the step of transforming, with the recombinant virus and recombinant virus vector, at least one kind of a host cell selected from the group consisting of a T cell, macrophage, peripheral-blood mononuclear cell, blood stem cell, liver

cell, vascular endothelial cell, fibroblast, glial cell, astrocyte, CD4 positive T cell, CD8 positive T cell, dendritic cell, and natural killer cell.

Conventionally, these cells had the problem of transfection efficiency and expression when used with conventional vectors. With a recombinant virus vector of the present invention, foreign genes can be introduced into these cells and expressed therein.

The transformation step may be performed either ex vivo or in vivo.

<Transformed Host Cells>

A transformed host cell of the present invention is obtained by the foregoing method of transforming a host cell.

A transformed host cell of the present invention may be used in gene therapy methods of mammals. The gene therapy for which a transformed host cell of the present invention is used may be gene therapy (i) for preventing human immunodeficiency virus (HIV) infection in a compromised cell caused by HIV, and/or (ii) for immunotherapy of cancer.

Further, the host cell may be derived from a mammal of the kind subjected to the gene therapy.

<Gene Therapy Method>

A gene therapy method of the present invention is

for non-human mammals, and it includes the step of administering the transformed cell into such mammals.

A gene therapy method of the present invention may be used not only for gene therapy but also for virus therapy and cell therapy as well. The cell therapy refers to a method in which a cell that has been transformed by gene transfection is administered to a patient. The virus therapy refers to a method in which a patient is administered with a virus that is infectious and is intended to multiply inside the human body.

A gene therapy method of the present invention is for non-human mammals, and includes the step of transforming, with use of the recombinant virus and recombinant virus vector, a host cell inside the body of the mammal at a multiplicity of infection (MOI) of 0.01 to 20.

A gene therapy method of the present invention may include the step of expressing a gene encoded by an exogenous nucleotide sequence included in the recombinant virus and recombinant virus vector.

The following will describe the present invention in more detail based on Examples. It should be noted however that the present invention is not limited in any way by the following description.

The following Examples were carried out with

samples obtained with the informed consent of the blood donors who participated in the study.

<Construction of HHV-6 Recombinant Virus Vector H6R28>

In order to construct recombinant virus H628R, a U3-U7 gene cluster of human herpesvirus 6 (HHV-6) was replaced with EGFP-puro, a gene cassette containing the gene for enhanced green fluorescent protein (EGFP) under control of the human cytomegalovirus major immediate-early enhancer-promoter (MIEP) and the puromycin resistance gene under control of the simian virus 40 (SV40) early promoter. To insert the EGFP-puro cassette into the HHV-6 genome by homologous recombination, 1-kb segments of viral genome were inserted into each end of the cassette (Fig. 1).

The following gene clusters were examined: the DR2-DR7 genes, which are duplicated in the viral genome; U95, the positional homologue of the murine cytomegalovirus (MCMV) immediate-early (IE) 2 gene, which is known to be dispensable for viral replication; and the U3-U7 genes. Of these, it was found that replacement of the U3-U7 genes with EGFP-puro resulted in a successfully replicating virus.

The following specifically describes the construct procedure.

Figure 1 schematizes a structure of the recombinant virus H6R28.

At the top is a map of the HHV-6B HST genome, with the region U1 to U9 expanded below (in the middle).

In the recombinant virus vector H6R28, shaded arrows in the middle show the U3-U7 open reading frames replaced by the EGFP-puro cassette.

The bottom diagram represents pU2-U8 EGFP-puro, a plasmid for homologous recombination in which U2 DNA fragments and U8 DNA fragments used for homologous recombination are inserted at the both ends of the EGFP-puro cassette.

The annealing sites of the primers used are depicted by small arrows pointing left or right. The recognition sites of the restriction enzymes used are depicted by small arrows pointing upward or downward. The sizes of the amplified or digested fragments are indicated by dotted arrows.

The EGFP gene and HCMV MIEP of the EGFP-puro cassette were derived from pEGFP-C1 (nucleotide numbers 8 to 1640) (Clontech). Multiple cloning sites of pEGFP-C1 including PstI were deleted.

The puromycin-N-acetyl-transferase gene (pac) and SV40 early promoter gene of the EGFP-puro cassette were derived from pPUR (nucleotide numbers 408 to 1392)

(Clontech).

For the construct, the U2 gene was amplified by PCR with primers U2 XbaI and U2 AflII, and the U8 gene was amplified with U8 BamHI and U8 EcoRI. After a restriction enzyme digestion, the digested products were inserted into each end of pEGFP-puro to obtain pU2-U8 EGFP-puro.

The cloned plasmid pU2-U8 EGFP-puro was introduced into phytohemagglutinin (PHA)-stimulated peripheral blood mononuclear cells by using a Nucleofector™ electroporator (Amaxa Biosystems, Germany) according to the manufacturer's recommended protocol.

Briefly, 5×10^6 cells were mixed with 5 μ g of the plasmid and 100 μ l of Nucleofector™ solution for T cells, and electroporation was performed with the Nucleofector™ using the program U-14.

Alternatively, a conventional electroporation method was used. In this case, 1×10^7 cells were mixed with 50 μ g of the plasmid suspended in 500 μ l of K-phosphate-buffered saline (30.8 mM NaCl, 120.7 mM KCl, 8.1 mM Na_2HPO_4 , 1.46 mM KH_2PO_4 , and 25 mM MgCl_2), and the mixture was placed in an electroporation cuvette (Gene Pulser cuvette, 0.4-cm diameter; Bio-Rad).

Electroporation was performed with a Gene Pulser II

electroporation system (Bio-Rad) with resistance at infinity, voltage at 300 V, and capacitance at 960 μ F. After 6 hours, the cells were infected with HHV-6 variant B of the HST strain at a multiplicity of infection (MOI) of 0.5 using the centrifuge method.

Cells were cultured for 3 days in RPMI 1640 supplemented with 10% fetal bovine serum and frozen as a virus stock. To enrich for the recombinant virus, PHA-stimulated umbilical cord blood mononuclear cells (CBMCs) were infected with the virus stock and cultured for 1 day, treated with 7.5 μ g of puromycin/ml for 1 day, washed with the medium, and cultured with CBMCs for 3 days. The infected cells were then frozen as a new virus stock.

This selection procedure was repeated five times, and the recombinant virus (H6R28) was subsequently cloned by limiting dilution using CBMCs cultured in 96-well plates.

<Construction Confirmation of HHV-6 Recombinant Virus Vector H6R28>

To confirm the insertion of the EGFP-puro cassette into the expected region, viral DNA was amplified by double-nested PCR with KOD Plus DNA polymerase (TOYOBO, Otsu, Japan) using primers against regions outside the homologous hinge regions (outer primer set

U2R2-U8F2 and inner primer set U2R1-U8F1) (Fig. 1).

The amplified products were subjected to electrophoresis. As the gel, 0.6% agarose gel was used. The results are shown in Figure 2(A). An amplified product of approximately 8.5 kb was observed in the wild-type (wt) virus (lane 1), conforming to the expected value (open arrow in Figure 2(A)). An amplified product of approximately 5.0 kb was observed in H6R28 (lane 2), conforming to the expected value (solid arrow in Figure 2(A)). Note that, the 5.0-kb bands were observed in three clones of H6R28.

The amplified products were confirmed by partial sequencing (data not shown). The 8.5-kb product was not observed in the recombinants, which indicated that they were not contaminated with the wt virus.

The amplified products were digested with the restriction enzymes (PstI, AflII, and BamHI) (Figure 1), and were subjected to 1.0% agarose gel electrophoresis. The results are shown in Figure 2(B). In Figure 2(B), open arrows on the left-hand side depict the expected sizes of the digested fragments in the wt virus, and solid arrows in the right-hand side depict the expected sizes of the digested fragments in H6R28. As Figure 2(B) clearly shows, the treatment of the amplified products with the restriction enzymes gave rise to the expected bands in

both wt virus (lane 1) and H6R28 (lanes 4-6).

The inserted position of EGFP-puro was also examined. Specifically, PCR was run with a primer U2R1-EGFPprim and a primer U8F1-PACprim, using DNA of H6R28 as a template. The amplified products were subjected to 1.0% agarose gel electrophoresis.

The results are shown in Figure 2(C). Solid arrows on the right-hand side depict the expected size (1582 bp) of the fragment amplified by the primer U2R1-EGFPprim, and the expected size (1760 bp) of the fragment amplified by the primer U8F1-PACprim. As Figure 2(C) clearly shows, bands of the expected sizes were obtained in both the fragment amplified with the primer U2R1-EGFPprim (lane 1), and the fragment amplified with the primer U8F1-PACprim (lane 2).

The possibility of the ectopic expression of U3-U7 genes was addressed. Specifically, an attempt was made to amplify the respective open reading frames of the U3 to U7 genes in which EGFP-puro has supposedly replaced the ORF. PCR was run using the wt viral DNA or H6R28 DNA as a template. For the amplification of U3, U4, U5, U6, and U7, the primer pairs U3F1-U3R1, U4F1-U4R1, U5F1-U5R1, U6F1-U6R1, and U7F1-U7R1 were used, respectively. The PCR products were subjected to 1.0% agarose gel electrophoresis.

The results are shown in Figure 2(D). Solid arrows on the left-hand side and right-hand side depict the expected sizes of the fragments amplified by the primer pairs. The sizes of U3F-U3R, U4F-U4R, U5F-U5R, U6F-U6R, and U7F-U7R were 1161 bp, 1338 bp, 1275 bp, 171 bp, and 1094 bp, respectively.

As Figure 2(D) clearly shows, the wt virus (lanes 1-5) gave rise to fragments of sizes as expected from the respective primer pairs. In H6R28 (lanes 6-10), no amplified fragments were detected.

<Productive Infection of HHV-6 Recombinant Virus Vector H6R28>

The inventors of the present invention produced three independent isolates of H6R28 by three individual electroporations and examined the replication kinetics in CBMCs. Virus titration was performed using CBMCs according to the method of Asada et al. (H. Asada, et. al, J. Clin. Microbiol. 27:2204-2207, 1989) as described above. CBMCs were infected at a MOI of 0.05, and the three H6R28 clones and the wt virus showed similar levels of viral spreading (Figure 3(A)) and virus production (Figure 3(B)) over time.

Figure 3 a graph representing productive infection of H6R28.

Figure 3(A) represents kinetics of the increase in

cells infected with wt virus and H6R28. CBMCs were infected with wt virus and three independent clones of H6R28 at an MOI of 0.05 (50% tissue culture infectious doses (TCID₅₀)/cell), and the percentages of cells reacting with a mixture of monoclonal antibodies to glycoprotein B and glycoprotein H were determined by IFA staining using monoclonal antibodies. The percentages of cells infected with wt virus (open circle), H6R28 clone 1 (solid triangle), clone 2 (solid circle), and clone 3 (solid square) are shown. Data shown are mean values of results for three replicate cultures.

Figure 3(B) represents growth curves for wt virus and H6R28.

CBMCs were infected as described above, and infected cells were harvested at the indicated times and frozen at -80°C. Progeny viruses were titrated on CBMCs using IFA staining. Virus titer was indicated as 50% TCID per milliliter. Titers from cells infected with wt virus (open square), H6R28 clone 1 (solid triangle), clone 2 (solid circle), and clone 3 (solid square) are shown. Values on day 0 represent the titers of the input viruses. Data shown are mean values of results for three replicate cultures.

It was found from the results shown in Figure 3(A) and Figure 3(B) that H6R28 had the same level of

proliferation as the wt virus. In other words, it was found that the insertion of foreign genes at the U2 to U8 sites had no effect on virus proliferation.

<Construction of HHV-6 Recombinant Vector H6R24-25>

Recombinant virus vector H6R24-25 was constructed that used the U24 and U25 regions of HHV-6 as recombinant sites.

Figure 4 schematizes a structure of the recombinant virus H6R24-25.

At the top is a map of the HHV-6B HST genome, with the regions U24 and U25 expanded below (in the middle).

The bottom diagram represents pHHV-6 U24-U25 EGFP-IRES-puro, a plasmid for homologous recombination in which U24 DNA fragments and U25 DNA fragments used for homologous recombination are inserted at the both ends of the EGFP-puro cassette.

The annealing sites of the primers used are depicted by small arrows pointing left or right.

The numbers 36250, 36980, and 37775 are the base numbers of the HHV-6HST strain.

In order to allow genes to be inserted in shorter recombinant sites than those of the recombinant virus H6R28, the size of genes was reduced using internal ribosomal entry site (IRES).

The construct procedure was the same as for H6R28 except that primers U24 SpeI and U25 EcoRI and primers U25 MluI and U25 KpnI were used for the amplification of U24 and U25 genes used for homologous recombination.

Confirmation of the H6R24-25 construct was made in the manner described in conjunction with the H6R28 construct. The same results were obtained. To avoid redundancy, no further explanation will be made.

As with the H6R28, H6R24-25 was examined in regard to the efficiency of viral spreading among cells and the efficiency of virus production in the infected cells. The experiment method was the same as that for H6R28.

Figure 5(A) represents an increase in virus antigen positive cells. Figure 5(B) represents a growth curve of the virus. In Figures 5(A) and 5(B), open circle denotes the wt virus, and solid square represents H6H24-25.

It was found from the results shown in Figure 5(A) and Figure 5(B) that H6R24-25 had the same level of proliferation as the wt virus. In other words, it was found that the insertion of foreign genes at the U24 and U25 sites had no effect on virus proliferation.

It was found from the data of H6R28 and H6R24-25 that, in HHV-6, the U3, U4, U5, U6, U7, U8, U24, and U25 regions were usable as the insertion sites of foreign genes.

<Latent Infection Ability and Reactivation Efficiency
of HHV-6 Recombinant Virus Vector>

The inventors of the present invention investigated H6R28 for its ability to establish latency and its efficiency of reactivation.

To evaluate the establishment of latency, peripheral blood macrophages were infected with wt virus and H6R28 and the percentage of HHV-6 DNA-positive cells was monitored according to method described in Kondo et al. (J. Gen. Virol.72: 1401-1408, 1991, J. Virol.77: 2258-2264, 2003, J. Virol.76: 4145-4151, 2002).

Briefly, peripheral blood macrophages were cultured in RPMI 1640 supplemented with 25% horse serum on plastic plates coated with collagen (Sumitomo Bakelite Co., Ltd. Japan).

The macrophages were infected with HHV-6 on day 7 and cultured for 4 to 6 weeks. The infected macrophages were detached from the plates, and the absence of viral replication was confirmed by immunofluorescent antibody (IFA) staining using monoclonal antibodies against glycoproteins B and H.

The cells were serially diluted (10^4 to 1 cell per tube) into sample tubes using four tubes for each dilution, and the DNA was isolated from each sample tube. Viral DNA was detected by double-nested PCR (K Kondo, et. al, J.

Infect. Dis. 167:1197-1200, 1993), and the numbers of HHV-6 DNA positive cells were calculated by the Reed-Muench method (Reed, L. J., and H. Muench, Am. J. Hyg. 27:493, 1938).

To study the reactivation efficiency, viral reactivation was induced by tetradecanoyl phorbol acetate (TPA) treatment according to the method described in Kondo et al. (J. Gen. Virol. 72: 1401-1408, 1991, J. Virol. 76: 4145-4151, 2002). Briefly, latently infected cells were detached from the culture dish, serially diluted, and cocultivated with an uninfected macrophage feeder layer. Subsequently, the cells were treated with TPA (20 ng/ml) for 7 days and cocultivated with CBMCs for 7 days. The efficiency of the viral reactivation was calculated by the Reed-Muench method (Reed, L. J., and H. Muench, Am. J. Hyg. 27: 493, 1938).

The results are shown in Figures 6(A) and 6(B).

Figure 6(A) represents percentages of HHV-6 DNA-positive cells. The percentages of HHV-6 DNA positive cells were examined 4 and 6 weeks postinfection. The data shown are mean values and standard deviations of results for three replicate cultures of wt virus and three clones of H6R28. Open column indicates wt virus. Shaded column indicates H6R28.

Figure 6(B) represents percentages of reactivation

positive cells. Viral reactivation was induced, and the percentages of reactivation-positive cells were calculated. The data shown are mean values and standard deviations of results for three replicate cultures of wt virus and three clones of H6R28. Open column indicates wt virus. Shaded column indicates H6R28.

As is clear from Figure 6(A) and Figure 6(B), the percentages of HHV-6 DNA positive cells and reactivation positive cells were found to be similar for the wt virus and H6R28. From these data, it was concluded that the establishment of latency and the reactivation process were not impaired by the deletion of the U3-U7 genes.

<Transfection of Various Cells with HHV-6 Recombinant Virus Vector>

(1) Macrophage, CBMCs, Molt-3, HeLa

Interestingly, during HHV-6 latency, the inventors of the present invention failed to detect the expression of EGFP that was driven by the HCMV major immediate-early enhancer-promoter (MIEP) (Figure 7(A)). On the other hand, EGFP expression was observed in the latently infected macrophage (Figure 7(B)) transfected with the plasmid pU2-U8 EGFP-puro illustrated in Figure 1, reactivation-induced macrophages (Figure 7(C)), productively infected CBMCs and Molt-3 cells (Figures 7(D) and 7(E)), and abortively infected HeLa cells (Figure

7(D)).

Figure 7 represents fluorescence micrographs showing EGFP expression in various types of cells. In Figure 7, cultured live cells were observed under fluorescent illumination.

Figure 7(A) shows macrophages that were latently infected with H6R28. Figure 7(B) shows latently infected macrophages that were transfected with the plasmid pU2-U8 EGFP-puro shown in Fig. 1 (transfection was performed according to the method described in Kondo et al. (J. Virol.77: 2258-2264, 2003)). Figure 7(C) shows reactivation-induced macrophages that were treated with 20 ng of TPA/ml for 7 days.

Figure 7(D) shows CBMCs infected with H6R28. Figure 7(E) shows Molt-3 cells infected with H6R28. Figure 7(F) shows HeLa cells infected with H6R28.

The cells were observed 4 weeks (A to C) or 2 days (E to F) postinfection. The transfected cells were observed 1 day post transfection (B).

(2) Natural Killer (NK) Cells

Adult peripheral blood mononuclear cells cultured in the presence of interleukin-2 (IL-2) were infected with the free virus of H6R28 at a multiplicity of infection (MOI) 1. Gene transfection in the CD56 positive cells (NK cells) was confirmed through EGFP expression, using FACS on

day 3 postinfection.

The results are shown in Figures 8(A) through Figure 8(C). Figure 8(A) shows the result for cells uninfected with H6R28. Figure 8(B) shows the result for cells infected with H6R28. Figure 8(C) is a graph summarizing the results shown in Figures 8(A) and 8(B).

As is clear from Figures 8(A) through 8(C), HHV-6 allowed for efficient transfection of the NK cells with foreign gene EGFP. The transfection rate was 88% $[39.8\% / (5.5\% + 39.8\%)]$.

(3) Astrocytes

The primary culture of human astrocytes cultured in the presence of a basic fibroblast growth factor (bFGF) was infected with the free virus of H6R28 at a multiplicity of infection (MOI) 1. Gene transfection was confirmed through EGFP expression on day 2 postinfection, using a fluorescent microscope.

Figure 9 represents the fluorescence micrograph. HHV-6 allowed about 40% of the primary culture of human astrocytes to be transfected with foreign gene EGFP.

(4) CD4 positive T cells

Adult peripheral blood mononuclear cells cultured in the presence of phytohemagglutinin (PHA) was infected with the free virus of H6R28 at a multiplicity of infection

(MOI) 1. Gene transfection was confirmed through EGFP expression on day 1 postinfection, using FACS.

Figure 10 shows the result. HHV-6 allowed for transfection of about 30% [$19.6\% / (50.8\% + 19.6\%)$] of the CD4 positive T cells with foreign gene EGFP.

(5) CD8 positive T cells

Adult peripheral blood mononuclear cells cultured in the presence of phytohemagglutinin (PHA) was infected with the free virus of H6R28 at a multiplicity of infection (MOI) 1. Gene transfection was confirmed through EGFP expression on day 3 postinfection, using FACS.

Figure 11 shows the result. HHV-6 allowed for transfection of about 40% [$30.1\% / (38.3\% + 30.1\%)$] of the CD8 positive T cells with foreign gene EGFP.

(6) Dendritic Cells

Adult peripheral blood mononuclear cells cultured in the presence of interleukin-4 (IL-4) and granulocyte-macrophage colony-stimulating factor (GM-CSF) was infected with the free virus of H6R28 at a multiplicity of infection (MOI) 1. Gene transfection of the CD83 positive cells (dendritic cells) was confirmed through EGFP expression on day 3 postinfection, using FACS.

Figure 12 shows the result. HHV-6 allowed for transfection of about 60% [$43.2\% / (26.6\% + 43.2\%)$] of the

CD83 positive dendritic cells with foreign gene EGFP.

Note that, though no Examples are given, there have been reports that the wt HHV-6 also infects blood stem cells, liver cells, vascular endothelial cells, and fibroblasts (see Reference Documents 1 - 5), suggesting that the H6R28 free virus can also infect these types of cells.

(Reference Document 1)

Luppi M, Barozzi P, et. al, J Virol., January, 1999, Vol. 73, No. 1, P. 754-9. "Human herpesvirus 6 latently infects early bone marrow progenitors in vivo"

(Reference Document 2)

Tajiri H, Tanaka-Taya K, et. al, Pediatr., September 1997, Vol. 131, No. 3, p. 473-5. "Chronic hepatitis in an infant, in association with human herpesvirus-6 infection"

(Reference Document 3)

Wu CA, Shanley JD., March 1998, Vol. 79, No. 5, p. 1247-56. "Chronic infection of human umbilical vein endothelial cells by human herpesvirus-6"

(Reference Document 4)

Rotola A, Di Luca D, et. al, J Clin Microbiol., August 2000, Vol. 38, No. 8, p. 3135-6. "Human herpesvirus 6 infects and replicates in aortic endothelium"

(Reference Document 5)

Luka J, Okano M, Thiele G., J Clin Lab Anal., April 1990, Vol. 4, No. 6, p. 483-6. "Isolation of human herpesvirus-6 from clinical specimens using human fibroblast cultures"

<Function of HCMV Promoter in Latently Infected HHV-6>

To investigate the gene expression from the IE1/IE2 promoter, 5' RACE was performed (J. Virol.77: 2258-2264, 2003, J. Virol.76:4145-4151, 2002, Proc. Natl. Acad. Sci.USA, 93: 11137-11142, 1996).

Briefly, the 5' end of the cDNA was dA tailed and annealed with an anchor primer, RL-1. The initial 10 cycles of PCR were performed with Taq polymerase (Roche Diagnostics) using the following conditions: denaturation for 1 min at 94°C, annealing for 1 min at 55°C, and extension for 1 min at 72°C.

PCR amplification was performed with PCR with KOD Plus DNA polymerase (TOYOBO, Otsu, Japan) using primers N1 and EGFP-R1 followed by primers N2 and EGFP-R2 (Figure 13(A)) under the following conditions: denaturation for 1 min at 94°C, annealing for 30 sec. at 65°C, and extension for 1 min at 68°C (15 cycles per amplification). The amplified products were sequenced.

In the latent cells, transcription of the mRNA from the usual transcription start position (productive

infection transcription start site [PSS]) was not detected (Figure 13(B)); however, small amounts of mRNA were transcribed from the latent infection transcription start sites (LSSs) 1 and 2 of HCMV, which are used to express the latency-associated transcripts of HCMV.

In contrast, the PSS was used in the latently infected macrophage transfected with the plasmid pU2-U8 EGFP-puro, reactivation-induced macrophages, and the productively infected Molt-3 cells and the abortively infected HeLa cells (Figure 13 (B)). Since HCMV MIEP showed the latency-associated performance in the context of HHV-6 latency, it is suggested that the transcriptional control of HHV-6 latency may share some common mechanism with HCMV latency. These findings may be related to the fact that HCMV shows some similarity with HHV-6, such as the site of latency.

Figure 13 is a schematic diagram and an electrophoretogram showing functions of the HCMV promoter in the latently infected HHV-6.

Figure 6(A) shows HCMV IE1/IE2 promoter and PCR primers. The EGFP gene and transcription start sites are drawn to scale. The PSS of IE1/IE2 mRNA (indicated as +1) and two LSSs (LSS1 and LSS2) are shown. The locations of the PCR primers are depicted, and a schematic drawing shows the usage of the anchor primer

RL-1. Primer sequences are shown in Table 1.

Figure 6(B) represents 5' RACE amplification of the EGFP transcripts.

Lane 1 shows RNA from 1×10^5 latently infected macrophages (Mf). Lane 2 shows 1×10^5 latently infected macrophages that were transfected with the plasmid pU2-U8 EGFP-puro shown in Figure 1. Lane 3 shows 1×10^5 reactivation-induced macrophages. Lane 4 shows 1×10^2 productively infected Molt-3 cells. Lane 5 shows 1×10^3 abortively infected HeLa cells.

These cells were analyzed by the 5' RACE method. The RACE method used was the same as that commonly used. The 5' end of the transcript was dA tailed and annealed with the anchor primer RL-1 (Fig. 6A) and amplified first with primers N2-EGFP R2 and then with primers N1-EGFP R1. The 5' ends of the transcript initiating at PSS (up to 360 bp), LSS1 (up to 720 bp), and/or LSS2 (up to 650 bp) were detected. HaeIII-digested Φ X174 DNA fragments were used as size markers (Φ X).

<Construction of HHV-7 Recombinant Virus Vector H7R28>

In order to construct recombinant virus H7R28, a U2-U8 gene cluster of human herpesvirus 7 (HHV-7) was replaced with EGFP-puro, a gene cassette containing the gene for enhanced green fluorescent protein (EGFP) under

control of the human cytomegalovirus major immediate-early enhancer-promoter (MIEP) and the puromycin resistance gene under control of the SV40 early promoter. To insert the EGFP-puro cassette into the HHV-7 genome by homologous recombination, 1-kb segments of viral genome were inserted into each end of the cassette (Fig. 14).

The U2-U8 gene clusters were examined. It was found that replacement of the U2-U8 genes with EGFP-puro resulted in a successfully replicating virus.

The following specifically describes the construct procedure.

Figure 14 schematizes a structure of the recombinant virus H7R28.

At the top is a map of the HHV-7 RK genome, with the region U2 to U8 expanded below (in the middle).

The bottom diagram represents HHV-7 pU2-U8 EGFP-puro, a plasmid for homologous recombination in which DNA fragments used for homologous recombination are inserted at the both ends of the EGFP-puro cassette.

The annealing sites of the primers used are depicted by small arrows pointing left or right.

The numbers 10558, 11637, and 18483 are the base numbers of the HHV-7RK strain.

Primer sequences are shown in Table 2 below.

[Table 2]

PRIMER	SEQ ID NO:	PRIMER SEQUENCE
7U2F1	28	5'- CAGCGTTTCCTGATGTTGGAACCCAG -3'
7U2R1	29	5'- GCATCTTACCAATGATGATCGCAAGC -3'
7U2FBam	30	5'- TTGGATCCTGATCATTTGCATGTTGCTAGTATGTCAG -3'
7U2RSpe	31	5'- GACTAGTCTCCGAATCGAAGCTAATCTGAGAGC -3'
7U8F1	32	5'- CCGATTCCTACTTTTCGACAAGAGG -3'
7U8R1	33	5'- CTCCGTACCACAGTCTGTCTAGCTC -3'
7U8FSal	34	5'- GCGTCGACAGCCAGTTGACGTTGCTGGTTACTCAG -3'
7U7RBam	35	5'- TTGGATCCATGCCTTCTCCATATGAAGACAGCAGC -3'
7U24 Spe I	40	5'- GGACTAGTCACTGCGCAATTAGAAGAAGCCTAG -3'
7U25 Eco RI	41	5'- GGAATTCGATGATGAACAAATCATTTTTCTCGCAC -3'
7U25 Mlu I	42	5'- CGACGCGTCACCAAAAATTTCCCATTCACATCG -3'
7U25 Kpn I	43	5'- GGGGTACCGCATGGATTTCTTAGCGAATTTGTGCTG -3'

For the construct, the U2 gene was amplified by PCR with primers 7U2FBam and 7U2RSpe, and the U7-U8 genes were amplified with primers 7U8FSal and 7U7RBam.

The amplified U2 gene product was digested with SpeI-BamHI. The amplified U7U8 gene product was digested with SalI-BamHI. The digested products were then inserted into each end of pEGFP-puro (HHV-7 pU2-U8 EGFP-puro in Figure 14).

The cloned plasmid HHV-7 pU2-U8 EGFP-puro was transfected into phytohemagglutinin (PHA)-stimulated peripheral blood mononuclear cells (PBMCs) by using a

Nucleofector™ electroporator (Amaxa Biosystems, Germany) according to the manufacturer's recommended protocol.

Briefly, 5×10^6 cells were mixed with 5 μ g of the plasmid and 100 μ l of Nucleofector™ solution for T cells, and electroporation was performed with the Nucleofector™ using the program U-14.

Alternatively, a conventional electroporation method was used. In this case, 1×10^7 cells were mixed with 50 μ g of the plasmid suspended in 500 μ l of K-phosphate-buffered saline (30.8 mM NaCl, 120.7 mM KCl, 8.1 mM Na_2HPO_4 , 1.46 mM KH_2PO_4 , and 25 mM MgCl_2), and the mixture was placed in an electroporation cuvette (Gene Pulser cuvette, 0.4-cm diameter; Bio-Rad).

Electroporation was performed with a Gene Pulser II electroporation system (Bio-Rad) with resistance at infinity, voltage at 300 V, and capacitance at 960 μ F. After 6 hours, the cells were infected with HHV-7 KHR strain at a multiplicity of infection (MOI) of 0.5 using the centrifuge method.

Cells were cultured for 3 days in RPMI 1640 supplemented with 10% fetal bovine serum and frozen as a virus stock. To enrich for the recombinant virus, PHA-stimulated umbilical cord blood mononuclear cells (CBMCs) were infected with the virus stock and cultured

for 1 day, treated with 7.5 µg of puromycin/ml for 1 day, washed with the medium, and cultured with CBMCs for 3 days. The infected cells were then frozen as a new virus stock.

This selection procedure was repeated five times, and the recombinant virus (H7R28) was subsequently cloned by limiting dilution using CBMCs cultured in 96-well plates.

<Construction Confirmation of HHV-7 Recombinant Virus Vector H7R28>

Construction of the HHV-7 recombinant virus vector was confirmed by the method used to confirm construction of the HHV-6 recombinant virus vector H6R28. The results were the same. To avoid redundancy, no further explanation will be made.

<Productive Infection of HHV-7 Recombinant Virus Vector H7R28>

H7R28 was examined in regard to the efficiency of viral spreading among cells and the efficiency of virus production in the infected cells. The experiment method was the same as that for H6R28, except that the anti-HHV-7 monoclonal antibody (KR4) was used instead of the anti-HHV-6 monoclonal antibody.

Figure 15(A) represents an increase in virus antigen positive cells. Figure 15(B) represents a growth curve of

the virus. In Figures 15(A) and 15(B), open circle denotes the wt virus, and solid square represents H7H28.

It was found from the results shown in Figure 15(A) and Figure 15(B) that H7R28 had the same level of proliferation as the wt virus. In other words, it was found that the insertion of foreign genes at the U2, U3, U4, U5, U7, and U8 sites had no effect on virus proliferation.

<Construction of HHV-7 Recombinant Vector H7R24-25>

Recombinant virus vector H7R24-25 was constructed that used the U24 and U25 regions of HHV-7 as recombinant sites.

Figure 16 schematizes a structure of the recombinant virus H7R24-25.

At the top is a map of the HHV-7 RK genome, with the regions U24 and U25 expanded below (in the middle).

The bottom diagram represents pHHV-7 U24-U25 EGFP-IRES-puro, a plasmid for homologous recombination in which DNA fragments used for homologous recombination are inserted at the both ends of the EGFP-puro cassette.

The annealing sites of the primers used are depicted by small arrows pointing left or right.

The numbers 34744, 35420, and 36118 are the base numbers of the HHV-7RK strain.

In order to allow genes to be inserted in shorter recombinant sites than those of the recombinant virus H7R28, the size of genes was reduced using internal ribosomal entry site (IRES).

The construct procedure was the same as for H7R28 except that primers U24 SpeI and U25 EcoRI and primers U25 MluI and U25 KpnI were used for the amplification of U24 and U25 genes used for homologous recombination.

Confirmation of the H6R24-25 construct was made in the manner described in conjunction with the H6R28 construct. The same results were obtained. To avoid redundancy, no further explanation will be made.

As with the H6R28, H7R24-25 was examined in regard to the efficiency of viral spreading among cells and the efficiency of virus production in the infected cells. The experiment method was the same as that for H6R28, except that the anti-HHV-7 monoclonal antibody (KR4) was used instead of the anti-HHV-6 monoclonal antibody.

Figure 17(A) represents an increase in virus antigen positive cells. Figure 17(B) represents a growth curve of the virus. In Figures 17(A) and 17(B), open circle denotes the wt virus, and solid square represents H7H24-25.

It was found from the results shown in Figure 17(A) and Figure 17(B) that H7R24-25 had the same level of proliferation as the wt virus. In other words, it was found

that the insertion of foreign genes at the U24 and U25 sites had no effect on virus proliferation.

It was found from the data of H7R28 and H7R24-25 that, in HHV-7, the U3, U4, U5, U7, U8, U24, U24a, and U25 regions were usable as the insertion sites of foreign genes.

<Latent Infection Ability and Reactivation Efficiency of HHV-7 Recombinant Virus Vector>

As with HHV-6 recombinant virus vector, HHV-7 recombinant virus vector was investigated for its ability to establish latency and its efficiency of reactivation. The method used for the HHV-6 recombinant virus vector was used, and the same results were obtained. To avoid redundancy, no further explanation will be made.

<Transfection of Various Cells with HHV-7 Recombinant Virus Vector>

(1) Macrophage

Adult peripheral blood mononuclear cells cultured in the collagen coat dish were infected with the free virus of H7R28 at a multiplicity of infection (MOI) 1. Gene transfection in the adhesive cell, i.e., CD11c positive cells (macrophage), was confirmed through EGFP expression, using FACS on day 3 postinfection.

The results are shown in Figure 18. HHV-7 allowed about 80% $[45.7\%/(12.1\%+45.7\%)]$ of the macrophage to

be transfected with foreign gene EGFP.

(2) CD4 positive T cells

Adult peripheral blood mononuclear cells cultured in the presence of phytohemagglutinin (PHA) was infected with the free virus of H7R28 at a multiplicity of infection (MOI) 1. Gene transfection in the CD4 positive T cells was confirmed through EGFP expression on day 3 postinfection, using FACS.

Figure 19 shows the result. HHV-7 allowed for transfection of about 48% [$34.8\% / (6.8\% + 34.8\%)$] of the CD4 positive T cells with foreign gene EGFP.

(3) Dendritic Cells

Adult peripheral blood mononuclear cells cultured in the presence of interleukin-4 (IL-4) and granulocyte-macrophage colony-stimulating factor (GM-CSF) was infected with the free virus of H7R28 at a multiplicity of infection (MOI) 1. Gene transfection of the CD83 positive cells (dendritic cells) was confirmed through EGFP expression on day 3 postinfection, using FACS.

Figure 20 shows the result. HHV-6 allowed for transfection of about 70% [$46.4\% / (17.9\% + 46.4\%)$] of the CD83 positive dendritic cells with foreign gene EGFP.

<Insertion of Replication Origins of BAC (Bacterial Artificial Chromosome) in HHV-6 and HHV-7>

The U2-U8 regions of HHV-6 and HHV-7 provide large insertion sites for foreign genes, and therefore allow relatively large genes to be transfected. Specifically, if the replication origins of bacterial artificial chromosome (BAC) could be inserted, then it would be possible to produce vectors according to a so-called BAC system. Production of recombinant virus by the BAC system has been established in many types of viruses, including other types of herpes viruses. However, there has been no established method in HHV-6 and HHV-7.

(1) Production of Recombinant HHV-6 with the Insertion of BAC Replication Origins (H6R28 BAC)

Figure 21 is a schematic diagram representing a structure of H6R28 BAC.

As in H6R28, the U2 and U8 sequences were used for homologous recombination. Plasmid pHHV-6 U2-8 EGFP-puro BAC was prepared in which BAC replication origins [chloramphenicol resistant gene (CMR), BAC replication origins (Ori S, rep E, par A, par B, par C)] were placed inside the homologous recombination sites. As the selection marker, EGFP and puromycin resistant gene (pac) ligated to each other with internal ribosomal entry site (IRES) were used.

The method of producing the virus by homologous recombination is the same as that described in

conjunction with the construction of H6R28. To avoid redundancy, no further explanation will be made.

The homologous recombination was followed by selection, which was carried out 6 times with puromycin. As a result, a recombinant virus with the BAC replication origins was produced.

The recombinant virus showed stable growth, and reached about 90% of the population after 6 rounds of puromycin selection. Figure 22 is a fluorescent micrograph showing Molt-3 cells infected with H6R28 BAC. The result shows that HHV-6 with the BAC replication origins was successfully produced by the foregoing method.

(2) Production of Recombinant HHV-7 with the Insertion of BAC Replication Origins (H7R28 BAC)

Figure 23 is a schematic diagram representing a structure of H7R28 BAC.

As in H7R28, the U2 and U8 sequences were used for homologous recombination. Plasmid pHHV-7 U2-8 EGFP-puro BAC was prepared in which BAC replication origins [chloramphenicol resistant gene (CMR), BAC replication origins (Ori S, rep E, par A, par B, par C)] were placed inside the homologous recombination sites. As the selection marker, EGFP and puromycin resistant gene (pac) ligated to each other with internal ribosomal

entry site (IRES) were used.

The method of producing the virus by homologous recombination is the same as that described in conjunction with the construction of H7R28. To avoid redundancy, no further explanation will be made.

The homologous recombination was followed by selection, which was carried out 6 times with puromycin. As a result, a recombinant virus with the BAC replication origins was produced.

The recombinant virus showed stable growth, and reached about 90% of the population after 6 rounds of puromycin selection. Figure 24 is a fluorescent micrograph showing SupT1 cells infected with H7R28 BAC. The result shows that HHV-7 with the BAC replication origins was successfully produced by the foregoing method.

<Summary of Evaluation Results>

Overall, the recombinant virus H6R28 revealed that the fairly large gene cluster U3-U7 was dispensable for viral replication, latency, and reactivation. Of the deleted genes, the characteristics of U4 and U6 have not been reported.

Similarly, the H7R28 revealed that the fairly large gene cluster U3-U7 was dispensable for viral replication, latency, and reactivation.

Genes U3, U5, U7, and U25 of HHV-6, and genes U3, U7, and U25 of HHV-7 belong to the US22 gene family, whose members are related to the HCMV US22 gene having the common motifs of unknown functions. Every betaherpesvirus encodes several US22 family genes that encode at least one of four conserved motifs. Although the functions of most of the US22 family genes are unknown, some of them, such as the murine cytomegalovirus (MCMV) immediate-early 2 (IE2) gene and the HCMV UL36-38 genes, encode proteins with transactivating functions.

However, MCMV IE2 is known to be dispensable for viral replication and latency and reactivation. Deletion of the US22 family genes of H6R28 showed them to have similar properties; HHV-6 U3 encodes a protein with a weak transactivating function, and the inventors of the present invention failed to find any difference in the viral replication or latency and reactivation between the wt and recombinant virus.

The US22 family genes UL36 and UL37 of HCMV have an antiapoptotic function. However, the inventors of the present invention did not observe increased apoptosis in H6R28- or H7R28-infected cells in the present study.

Other US22 family genes, such as the MCMV M140 and M141 genes, confer altered cell and tissue tropism.

Since the in vivo host tissue range of HHV-6 is broad and since the virus infects various types of cells, it is possible that the HHV-6 US22 family genes contribute to the broad organ tropism of this virus.

H6R28 appears to be a useful tool for the study of HHV-6 latency and reactivation. H7R28 appears to be a useful tool for the study of HHV-7 latency and reactivation. Moreover, in HHV-6 and HHV-7, this large dispensable locus can be a useful site for inserting a large gene, such as a bacterial artificial chromosome (BAC) vector. In fact, the inventors of the present invention have shown that the BAC gene can actually be stably inserted in HHV-6 and HHV-7.

It is believed that this is the first report of a successful recombinant HHV-6 virus vector and recombinant HHV-7 virus vector, and the invention can provide HHV-6 and HHV-7 investigators with a detailed protocol for making it.

The embodiments and concrete examples of implementation discussed in the foregoing detailed explanation serve solely to illustrate the technical details of the present invention, which should not be narrowly interpreted within the limits of such embodiments and concrete examples, but rather may be applied in many variations within the spirit of the present invention,

provided such variations do not exceed the scope of the patent claims set forth below.

INDUSTRIAL APPLICABILITY

A virus vector of the present invention (i) allows for insertion of an exogenous nucleotide sequence, (ii) can easily transfect a host cell of mammals, (iii) allows a gene encoded by the exogenous nucleotide sequence to be expressed in the host cell, (iv) has a low risk of pathogenicity, and therefore (v) is suitable for gene therapy of mammals.

A producing method of a virus vector of the present invention is for easily producing a virus vector that (i) allows for insertion of an exogenous nucleotide sequence, (ii) can easily transfect a host cell of mammals, (iii) allows a gene encoded by the exogenous nucleotide sequence to be expressed in the host cell, (iv) has a low risk of pathogenicity, and therefore (v) is suitable for gene therapy of mammals.

A method for making recombinant viruses, used in a producing method of a virus vector of the present invention is indispensable when other vector developing techniques such as the BAC system or amplicon system were to be applied to HHV-6 and HHV-7.

A transforming method of a host cell of the present

invention is a method for transforming a host cell with a virus vector that (i) easily allows for transfection of a mammalian host cell with an exogenous nucleotide sequence, (ii) allows a gene encoded by the exogenous nucleotide sequence to be expressed in the host cell, (iii) has a low risk of pathogenicity, and (v) therefore is suitable for gene therapy of mammals.

A transformed host cell of the present invention (i) is transformed with a virus vector with the insertion of an exogenous nucleotide sequence, (ii) allows a gene encoded by the exogenous nucleotide sequence to be expressed in the host cell, (iii) has a low risk of pathogenicity, and therefore (iv) can suitably be used for gene therapy.

A gene therapy method of the present invention is a gene therapy method for mammals using a virus vector that (i) easily allows for transfection of a mammalian host cell with an exogenous nucleotide sequence, (ii) allows a gene encoded by the exogenous nucleotide sequence to be expressed in the host cell, and (iii) has a low risk of pathogenicity.

Virus vectors of the present invention can be used for AIDS treatment by taking advantage of the fact that both HHV-6 and HHV-7 infect the CD4 positive T cells as does HIV. In this case, it is preferable that virus vectors of the present invention include anti-HIV genes such as

ribozyme and interference RNA.

Further, virus vectors of the present invention can be used for AIDS treatment by taking advantage of the fact that HHV-6 can latently infect macrophage as does HIV. In this case, it is also preferable that virus vectors of the present invention include anti-HIV genes such as ribozyme and interference RNA.

Further, virus vectors of the present invention can be used to introduce cytokine to the CD4 positive T cells, macrophage, natural killer cells, lymphokine activated killer (LAK) cells, and the like by taking advantage of the fact that both HHV-6 and HHV-7 infect the immunocompetent cells of these cells. Thus, virus vectors of the present invention can be used for the immunotherapy of cancer.

Further, virus vectors of the present invention are also applicable to anti-tumor treatment. In this case, pancreatic cancer cells are infected with HHV-6 to kill cancer cells, by taking advantage of the fact that HHV-6 can enter the cells by binding to CD46 molecules serving as receptors, which are abundantly expressed in pancreatic cancer cells or other refractory digestive system tumors.